

cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>

Plate: LNCM218 row: d column: 23
 High quality sequence stop: 670.
 Location/Qualifiers

FEATURES

source

1.1002
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5933542"
 /clone_id="NIH_MGC_106"
 /tissue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH MGC Library."
 BASE COUNT 221 a 296 c 288 g 197 t
 ORIGIN

Query Match 27.2%; Score 698; DB 14; Length 1002;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 748; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 350 CCAAGGCTTTGATGACAAACCAATTTCCCTGATGATGCTTCTGATGCTGCTGAG 409
 Db 31 CCAAGGCTTTGATGACAAACCAATTTCCCTGATGATGCTTCTGATGCTGCTGAG 90
 QY 410 GAAACAATGGGAAGTCTGCCAGCAGAGAAATCTGCCAAGCCCAAGCTTGAATTCCT 469
 Db 91 GAAACAATGGGAAGTCTGCCAGCAGAGAAATCTGCCAAGCCCAAGCTTGAATTCCT 150
 QY 470 CTGTCCAAAGGCGCAGGACCTGTGACCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 529
 Db 151 CTGTCCAAAGGCGCAGGACCTGTGACCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 210
 QY 530 CCTGGGAGAGTTTCCCGCAGGTGCGCCGCGCCGAGCTGTGCTGAGACTCGGGAGCCAT 589
 Db 211 CCTGGGAGAGTTTCCCGCAGGTGCGCCGCGCCGAGCTGTGCTGAGACTCGGGAGCCAT 270
 QY 590 TGACCATGCTCTGAGAGATGAGACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 649
 Db 271 TGACCATGCTCTGAGAGATGAGACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 330
 QY 650 AGTATAGACATCCCAAGGCTCAGCTGAGCCAAAGTCTCCATGAGGTGCTGTATAGAGGCC 709
 Db 331 AGTATAGACATCCCAAGGCTCAGCTGAGCCAAAGTCTCCATGAGGTGCTGTATAGAGGCC 390
 QY 710 TGAGCAGGAG 769
 Db 391 TGAGCAGGAG 450
 QY 770 TCATCCGAGAGAGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 829
 Db 451 TCATCCGAGAGAGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510
 QY 830 CTGCACTCTGGAGCCGATCAGACACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 889
 Db 511 CTGCACTCTGGAGCCGATCAGACACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 570
 QY 890 ACATCTCAACCGGCTTCACTTCCCTCACTCCAGGCGCTGTGAGACATTACTGTAGC 949
 Db 571 ACATCTCAACCGGCTTCACTTCCCTCACTCCAGGCGCTGTGAGACATTACTGTAGC 630
 QY 950 TGACGAGATGACATCTGCTGCTTCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1009

Db 631 TGCCGATGACATCTGCTGCTTCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
 QY 1010 TCCCTGGAGAGATATATACCTTCACTGATGATGATGATGATGATGATGATGATGATG 1069
 Db 691 TCCCTGGAGAGATATATACCTTCACTGATGATGATGATGATGATGATGATGATGATG 750
 QY 1070 AGCTGAG 1098
 Db 751 AGCTGAG 779

RESULT 3
 B677567 794 bp mRNA linear EST 01-MAY-2001
 LOCUS 602624118f1 NCI_CGAP_Skin4 Homo sapiens cDNA clone IMAGE:4748884.5',
 DEFINITION mRNA sequence.

ACCESSION B677567
 VERSION B677567
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 794)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-rc@mail.nih.gov
 Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>

Plate: LNCM218 row: d column: 05
 High quality sequence stop: 790.
 Location/Qualifiers

FEATURES

source

1.794
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4748884"
 /clone_id="NCI_CGAP_Skin4"
 /tissue_type="squamous cell carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 192 a 229 c 212 g 161 t
 ORIGIN

Query Match 24.6%; Score 631; DB 12; Length 794;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 946 GAGCTGCGGATGACATCTGCTGCTTCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1005
 Db 17 GAGCTGCGGATGACATCTGCTGCTTCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 76
 QY 1006 CCGCTCCCTGGCAAGATATACCCCTACCTGATCTGAGAGAGAGAGAGAGAGAGAGAGAG 1065
 Db 77 CCGCTCCCTGGCAAGATATACCCCTACCTGATCTGAGAGAGAGAGAGAGAGAGAGAGAG 136
 QY 1066 AAAAGGCTGAGACGCTCTCTGTTTCTGAAGCTGCCAAGAGAGAGAGAGAGAGAGAG 1125
 Db 137 AAAAGGCTGAGACGCTCTCTGTTTCTGAAGCTGCCAAGAGAGAGAGAGAGAGAGAG 196
 QY 1126 AGTGAAGGCTCTCGGAGAGTCCCTCAGCTTCAATCAGCTGAATGAAGAGAGAGAGAG 1185
 Db 197 AGTGAAGGCTCTCGGAGAGTCCCTCAGCTTCAATCAGCTGAATGAAGAGAGAGAGAG 256

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:

http://image.llnl.gov

Plate: L10M215 row: 3 column: 11

High quality sequence stop: 556.

FEATURES

Source

1. 1020

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5936362"

/clone_lib="NIH_MGC_106"

/tissue_type="natural killer cells, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT

ORIGIN

219 a 311 c 283 g 204 t 3 others

Query Match

Best Local Similarity

Matches 719; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

24.1%; Score 619; DB 14; Length 1020;

99.7%; Pred. No. 0;

0; Mismatches 2; Indels 0; Gaps 0;

0; Mismatches 2; Indels 0; Gaps 0;

0; Mismatches 2; Indels 0; Gaps 0;

0; Mismatches 2; Indels 0; Gaps 0;

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0; Mismatches 2; Indels 0; Gaps 0;

Db 665 |=====|

Qy 928 C 928

Db 725 C 725

FEATURES

Source

1. 1069

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5933772"

/clone_lib="NIH_MGC_106"

/tissue_type="natural killer cells, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT

ORIGIN

230 a 328 c 300 g 205 t 6 others

Query Match

Best Local Similarity

Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

23.6%; Score 605; DB 14; Length 1069;

100.0%; Pred. No. 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6

LOCUS

DEFINITION

AGNCOURT 6868422 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933772

5', mRNA sequence.

ACCESSION

KEYWORDS

SOURCE

ORGANISM

human.

human.

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EST 29-MAR-2002

linear

cdna

clone

image

5933772

5', mRNA sequence.

AGNCOURT 6868422 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933772

5', mRNA sequence.

AGNCOURT 6868422 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933772

5', mRNA sequence.

AGNCOURT 6868422 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933772

5', mRNA sequence.

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5', mRNA sequence.

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AGNCOURT 6868422 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933772

5', mRNA sequence.

AGNCOURT 6868422 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933772

Qy	567	GTGCGTGAAGCTCGGGGAGCAATTGACCAATCGCTCTTGAGAAATGAGACTGTGAGACGGT	626
Db	241	GTGCGTGAAGCTCGGGGAGCAATTGACCAATCGCTCTTGAGAAATGAGACTGTGAGACGGT	300
Qy	627	GCTGCTGAAGTCTCAGCGAAGATTAACATCCCAAGGCTCACTGGGCTCAAAATGTC	686
Db	301	GCTGCTGAAGTCTCAGCGAAGATTAACATCCCAAGGCTCACTGGGCTCAAAATGTC	360
Qy	687	CCATGGGTGCTGTATGAGGGCTTGACAGGGAGAAAGCAGAGAACTGCTGTGTTAAC	746
Db	361	CCATGGGTGCTGTATGAGGGCTTGACAGGGAGAAAGCAGAGAACTGCTGTGTTAAC	420
Qy	747	TGGGAACCCGTGAGGGGCTTCTCATCCGGGAGAGCAGACACAGAGAGGCTTTACTC	806
Db	421	TGGGAACCCGTGAGGGGCTTCTCATCCGGGAGAGCAGACACAGAGAGGCTTTACTC	480
Qy	807	TCTGTCAGTCCGCTTACGCCCTGTGATCTGGGACCGGATCAACACTACAGATCCA	866
Db	481	TCTGTCAGTCCGCTTACGCCCTGTGATCTGGGACCGGATCAACACTACAGATCCA	540
Qy	867	CTGCGCTTGACAAATGCGTGGCTGTACATCTCACCGAGGCTTACCTTCCCTCACTCCAGGC	926
Db	541	CTGCGCTTGACAAATGCGTGGCTGTACATCTCACCGAGGCTTACCTTCCCTCACTCCAGGC	600
Qy	927	CGTGG 931	
Db	601	CGTGG 605	

RESULT 7	854 bp	mRNA	linear	EST 16-FEB-2001
AL568702/c				
LOCUS	AL568702	L1_FLO02.PL1	Homo sapiens cDNA clone CSDBE005YK23	3 prime
DEFINITION	AL568702	1		
ACCESSION	AL568702			
VERSION	AL568702.1	GI:12923305		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
AUTHORS	Li W.B., Gruber C., Vessse, J. and Polayes D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Genoscope			

FEATURES

Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers

```

source
1. .854
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSDB005YK23"
/clone_lib="PTI Pl002_P11"
/lab_host="DH10B"
/notes="Organ, placenta, Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies, Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@life tech.com URL : http://fulllength.invitrogen.com"

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Query Match 23.4%; Score 600; DB 9; Length 854;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy	1841	TTTTTTTGAACAGCAGATCTTGCCCTGTCCTCCCAATGCTGAGGCAAGAGATCTCAG	1900
Db	602	TTTTTTTGAAGAGGAGTCTTGCCCTGTCCTCCCAATGCTGAGGCAAGAGATCTCAG	543
Oy	1901	CTCACTACGAACCTCAATCTCTGGATTTAAACAATTCCTGCTCAAGCTCCAAATAG	1960
Db	542	CTCACTCAACCTCCATCTCTGGATTTAAACAATTCCTGCTCAAGCTCCAAATAG	483
Oy	1961	CTGGGATTTACAGGCGTACACACATGCTGGCTAAATTTTTTGTATTTTATAGACAT	2020
Db	482	CTGGGATTTACAGGCGTACACACATGCTGGCTAAATTTTTTGTATTTTATAGACAT	423
Oy	2021	GGGGTTTCAACCAATTTGGCCAGGCTGTGTGAAATCTCGAACCTCAAGTGAATCAACCA	2080
Db	422	GGGGTTTCAACCAATTTGGCCAGGCTGTGTGAAATCTCGAACCTCAAGTGAATCAACCA	363
Oy	2081	CTTGGCTTCCCAAAATGTGTGGGATTCACAGGTGTAGCCACAGCACCCAGCTTACTCA	2140
Db	362	CTTGGCTTCCCAAAATGTGTGGGATTCACAGGTGTAGCCACAGCACCCAGCTTACTCA	303
Oy	2141	GATCTCTATTTTCATTTTGTGGCTTACATTTCCCTAGACACATGCGCTTGGCATCTTGGG	2200
Db	302	GATCTCTATTTTCATTTTGTGGCTTACATTTCCCTAGACACATGCGCTTGGCATCTTGGG	243
Oy	2201	CCGAATAAAAATTAACACTTCTTAAGCTTAGACACATGCAAGTGTGGCCAGGCACTCTAGT	2260
Db	242	CCGAATAAAAATTAACACTTCTTAAGCTTAGACACATGCAAGTGTGGCCAGGCACTCTAGT	183
Oy	2261	GCTGGGCAAGGGGATTCAGAAAGTGTCAAGCCCTCTCTCCAAATGCCAAGAGGAGACA	2320
Db	182	GCTGGGCAAGGGGATTCAGAAAGTGTCAAGCCCTCTCTCCAAATGCCAAGAGGAGACA	123
Oy	2321	CAGCCTACACAATATCAGCCCTTTGATTTTCCCTGCTCTCCATTAACAGAAAGAGTCT	2380
Db	122	CAGCCTACACAATATCAGCCCTTTGATTTTCCCTGCTCTCCATTAACAGAAAGAGTCT	63
Oy	2381	GCTGGATTCCTCTAAGGATTCAGGGAGAAAGAAAGAAAGGAGTGGGTGGAGGACCCCC	2440
Db	62	GCTGGATTCCTCTAAGGATTCAGGGAGAAAGAAAGAAAGGAGTGGGTGGAGGACCCCC	3

RESULT 8	LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM
AL844325	AL844325	pool_yt_11b_v	677 bp	EST 30-JUL-2002	Human	Homo sapiens
AL844325	AL844325	SPD Homo sapiens cDNA, mRNA sequence.				
AL844325.1	GI:22019105					
EST.						

TITLE Homo sapiens EST sequence
JOURNAL Unpublished (2002)
COMMENT Contact: The Sanger Centre
REFERENCE Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and Sheridan, E.
AUTHORS Ekuoyi, Y., Metaxas, C., Nozaki, C., Oatley, J., Vercellotti, Z., Zuercher, C., Mammali, J., Euthelia, L., Primates, C., Catarrhini, H., Homiidae, H., Homo, 1 (bases 1 to 677)

The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: hummerv@sanger.ac.uk
Sanger Centre name : sc001827_400489S
Homo sapiens EST sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA library
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cDNA clones derived from
pool YT lib v5 cDNA library. Further information can be found at
<http://www.sanger.ac.uk/Teams/Team9/>.

FEATURES
source
1..677
Location/Qualifiers

RESULT 10	AL844308/c	642 bp	mrna	linear	EST 30-JUL-2002
LOCUS	AL844308				
DEFINITION	AL844308 pool_AK_11b_v_SPD Homo sapiens		CDNA	MRNA	sequence.
ACCESSION	AL844308				
VERSION	AL844308.1	GI:22019990			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and Sheridan, E.				
TITLE	Homo sapiens EST sequence				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: The Sanger Centre The Sanger Centre Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK Email: humquery@sanger.ac.uk Sanger Centre name : sccdl0816.400489A Homo sapiens EST sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to identify and annotate genes in the human genome. Incomplete or unconfirmed genes are experimentally analysed using a variety of cDNA library resources. This sequence was obtained from a PCR product generated from a pool of up to 100,000 cDNA clones derived from pool_AK_11b_v_SPD cDNA library. Further information can be found at http://www.sanger.ac.uk/Teams/Team69/ Location/Qualifiers				
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	/map="20"				
	/clone_lib="pool_AK_11b_v_SPD"				
	/note="Organ: breast; Vector: pZERO-1; Site: 1: SpH1; Site 2: SpH1; Ductal carcinoma in situ, high-grade, comedo , from 41 yo female. Library constructed in the laboratory of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	http://www.sanger.ac.uk/Teams/Team69/				
	Location/Qualifiers				
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	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/map="20"				
	/clone_lib="pool_AK_11b_v_SPD"				
	/note="Organ: breast; Vector: pZERO-1; Site: 1: SpH1; Site 2: SpH1; Ductal carcinoma in situ, high-grade, comedo , from 41 yo female. Library constructed in the laboratory of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	http://www.sanger.ac.uk/Teams/Team69/				
	Location/Qualifiers				
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	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/map="20"				
	/clone_lib="pool_AK_11b_v_SPD"				
	/note="Organ: breast; Vector: pZERO-1; Site: 1: SpH1; Site 2: SpH1; Ductal carcinoma in situ, high-grade, comedo , from 41 yo female. Library constructed in the laboratory of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	http://www.sanger.ac.uk/Teams/Team69/				
	Location/Qualifiers				
	1..642				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/map="20"				
	/clone_lib="pool_AK_11b_v_SPD"				
	/note="Organ: breast; Vector: pZERO-1; Site: 1: SpH1; Site 2: SpH1; Ductal carcinoma in situ, high-grade, comedo , from 41 yo female. Library constructed in the laboratory of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	http://www.sanger.ac.uk/Teams/Team69/				
	Location/Qualifiers				
	1..642				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/map="20"				
	/clone_lib="pool_AK_11b_v_SPD"				
	/note="Organ: breast; Vector: pZERO-1; Site: 1: SpH1; Site 2: SpH1; Ductal carcinoma in situ, high-grade, comedo , from 41 yo female. Library constructed in the laboratory of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	http://www.sanger.ac.uk/Teams/Team69/				
	Location/Qualifiers				
	1..642				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/map="20"				
	/clone_lib="pool_AK_11b_v_SPD"				
	/note="Organ: breast; Vector: pZERO-1; Site: 1: SpH1; Site 2: SpH1; Ductal carcinoma in situ, high-grade, comedo , from 41 yo female. Library constructed in the laboratory of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."				
	http://www.sanger.ac.uk/Teams/Team69/				
	Location/Qualifiers				
	1..642				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/map="20"				

Db	288	TCGAGTCCCATATATCCCACTGCGACCTCTTAGTCAGTCAGACGAAAGAGGTGGACACGAGG	229
Qy	1445	TCAGAGTTCACAAAAGAAATTAAGCTCTCGGGGGGGCTCGACCTAGTTAGTCTTGAAGTT	1504
Db	228	CCAGGGTTCACAAAAGAAATTAAGCTCTCGGGGGGGGTGACCTAGTTAGTCTTGAAGTT	169
Qy	1505	TGGGGGTTTCAGATCACTCTGATGTCCTCGCTGTTGAAGCCCATCTTCAATCCCAACA	1564
Db	168	TGGGGGTTTCAGATCACTCTGATGTCCTCGCTGTTGAAGCCCATCTTCAATCCCAACA	109
Qy	1565	TTAACGAGGCCCCACCCACAGGTGTGAAGAACACC	1599
Db	108	TTAACGAGGCCCCACCCACAGGTGTGAAGAACACC	74
RESULT 11			
AL844326/C		599 bp	mRNA linear EST 30-JUL-2002
LOCUS	AL844326		
DEFINITION	AL844326		pool YT_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
ACCESSION	AL844326		
VERSION	AL844326.1		GI:22019106
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Ekaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
AUTHORS	Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and Sheridan, E.		
TITLE	Homo sapiens EST sequence		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: The Sanger Centre		
	The Sanger Centre		
	Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK		
	Email: humquery@sanger.ac.uk		
	Sanger Centre name: scd10827.dT		
	Homo sapiens EST sequence. This sequence was generated as part of		
	The Wellcome Trust Sanger Institute program to identify and		
	annotate genes in the human genome. Incomplete or unconfirmed genes		
	are experimentally analysed using a variety of cDNA library		
	resources. This sequence was obtained from a PCR product generated		
	from a pool of up to 100,000 cDNA clones derived from		
	pool YT_11b_v_SPD cDNA library. Further information can be found at		
	http://www.sanger.ac.uk/Teams/Team69/.		
FEATURES			
source	location/Qualifiers		
	1. 599		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/map="20"		
	/clone_11b="pool YT_11b_v_SPD"		
	/note="Organ: breast; Vector: pZero-1; Site_1: SphI;		
	Site_2: SphI; Ductal carcinoma in situ, high-grade, comedo		
	, from 41 yo female. Library constructed in the laboratory		
	of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."		
BASE COUNT	142 a 148 c 165 g 144 t		
ORIGIN			
Query Match	20.0%; Score 513; DB 9; Length 599;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 513; Conservative 0; Mismatches	0; Indels 0; Gaps		
Qy	1994	TAAATTTTGTATTTTGTATTTAGTAGACATGAGGTTTCAACATTTGGCAGGCTGTGTGCA	2053
Db	520	TAAATTTTGTATTTTGTATTTAGTAGACATGAGGTTTCAACATTTGGCAGGCTGTGTGCA	461
Qy	2054	ACTCTGACCTCAGGTGATCCACCCACTTGGCTCCCAAGTCTGGAGTTACAGGTGT	2113
Db	460	ACTCTGACCTCAGGTGATCCACCCACTTGGCTCCCAAGTCTGGAGTTACAGGTGT	401
Qy	2114	GAGCCAGGAGCCAGCCTGAGCTCTAGATCTCATTTATTTGTGGCTTACATTTCC	2173
Db	400	GAGCCAGGAGCCAGCCTGAGCTCTAGATCTCATTTATTTGTGGCTTACATTTCC	341

QY 2174 TAGCACTGGCTTGGCATCTTGGCCGAATAAATACCTCTTAAGCTACGA 2233
 DB 340 TAGCACTGGCTTGGCATCTTGGCCGAATAAATACCTCTTAAGCTACGA 281
 QY 2234 CACTGAGTGAAGCCAGGACCTGAGTCTGGGAGGGGATCAGAGAGTCTAAGCCCT 2293
 DB 280 CACTGAGTGAAGCCAGGACCTGAGTCTGGGAGGGGATCAGAGAGTCTAAGCCCT 221
 QY 2294 CTCTCCAGATGCCAAGACGAGACCAAGGCTCAGCAAAATCCAGCCCTGATTTCCCT 2353
 DB 220 CTCTCCAGATGCCAAGACGAGACCAAGGCTCAGCAAAATCCAGCCCTGATTTCCCT 161
 QY 2354 GCTGCTCCATTAACAGAAAGAGTCTGCTGATCCGCTTAAGGATCAGGAGAGAGA 2413
 DB 160 GCTGCTCCATTAACAGAAAGAGTCTGCTGATCCGCTTAAGGATCAGGAGAGAGA 101
 QY 2414 AAGAGGATGGGGTGGAGGACCCCTCCAGTCTCTCAATGCTTCCAGCTAAGCT 2473
 DB 100 AAGAGGATGGGGTGGAGGACCCCTCCAGTCTCTCAATGCTTCCAGCTAAGCT 41
 QY 2474 GGGGTGGAAAGCTTTATCAGGTATCATCAAC 2506
 DB 40 GGGGTGGAAAGCTTTATCAGGTATCATCAAC 8

RESULT 12
 BG284179 566 bp mRNA linear EST 21-FEB-2001
 LOCUS 602408226F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4520382 5',
 DEFINITION mRNA sequence.
 ACCESSION BG284179
 VERSION BG284179.1 GI:11034866
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 566)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: DCD/DTF
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM10418 row: c column: 07
 High quality sequence start: 2
 High quality sequence stop: 566.
 Location/Qualifiers
 source 1..566
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4520382"
 /clone_1lib="NIH_MGC_91"
 /issue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: prostate; Vector: pCMV-SPORT6, Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.4 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC library."
 BASE COUNT 116 a 187 c 152 g 110 t 1 others
 ORIGIN

QY 796 GGCTTTACTCTCTGCACTCCGCTCAGCCGCTTCATCTCCGGACCGGATCAGACAC 855
 DB 13 GGCTTTACTCTCTGCACTCCGCTCAGCCGCTTCATCTCCGGACCGGATCAGACAC 72
 QY 856 TACAGATTCACCTGCTTACAGATGAGCTGATCATCTCAGCCCTCAGCTTCCCT 915
 DB 73 TACAGATTCACCTGCTTACAGATGAGCTGATCATCTCAGCCCTCAGCTTCCCT 132
 QY 916 TACATCCAGGCTTGGTGGACCATTAATCTGAGCTGGGAGATGACATCTGCTTCT 975
 DB 133 TACATCCAGGCTTGGTGGACCATTAATCTGAGCTGGGAGATGACATCTGCTTCT 192
 QY 976 AAGAGCCCTGTCTCTGCAAGAGGCTGAGCCGCTCCCTGCAAGATATACCTACT 1035
 DB 193 AAGAGCCCTGTCTCTGCAAGAGGCTGAGCCGCTCCCTGCAAGATATACCTACT 252
 QY 1036 GTGATGTGCAAGAGCACCACTCACTGAGAGAGCTGACACTCTCTCTTTTCT 1095
 DB 253 GTGATGTGCAAGAGCACCACTCACTGAGAGAGCTGACACTCTCTCTTTTCT 312
 QY 1096 GAAGCTGCCAAGGAGAGAGTCTTCTCAGTGAAGGCTCCGAGAGTCCCTCAGCTTC 1155
 DB 313 GAAGCTGCCAAGGAGAGAGTCTTCTCAGTGAAGGCTCCGAGAGTCCCTCAGCTTC 372
 QY 1156 TACATCAGCTTGAATACAGAGCTGTCTCTTGGATGATGCTTGGCCCAAGAGAGGC 1215
 DB 373 TACATCAGCTTGAATACAGAGCTGTCTCTTGGATGATGCTTGGCCCAAGAGAGGC 432
 QY 1216 CAAAAGGAAACCAAGCTGCACACTTGAACCCCAATTCAGCTCTCTGGGCAACCCAGA 1275
 DB 433 CAAAAGGAAACCAAGCTGCACACTTGAACCCCAATTCAGCTCTCTGGGCAACCCAGA 492
 QY 1276 GGCAAGGC 1283
 DB 493 GGCAAGGC 500

RESULT 13
 AL844311 597 bp mRNA linear EST 30-JUL-2002
 LOCUS AL844311 pool_yt_1lb_v_SPD Homo sapiens cDNA, mRNA sequence.
 DEFINITION AL844311
 ACCESSION AL844311
 VERSION AL844311.1 GI:22019093
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 597)
 AUTHORS Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and
 Sheridan, E.
 TITLE Homo sapiens EST sequence
 JOURNAL Unpublished (2002)
 COMMENT Contact: The Sanger Centre
 The Sanger Centre
 Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: humuey@sanger.ac.uk
 Sanger Centre name: scc010818.154136A
 Homo sapiens EST sequence. This sequence was generated as part of
 The Wellcome Trust Sanger Institute program to identify and
 annotate genes in the human genome. Incomplete or unconfirmed genes
 are experimentally analysed using a variety of cDNA library
 resources. This sequence was obtained from a PCR product generated
 from a pool of up to 100,000 cDNA clones derived from
 pool YT_1lb v SPD cDNA library. Further information can be found at
 http://www.sanger.ac.uk/teams/team69/.
 Location/Qualifiers
 source 1..597
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="20"
 /clone_1lib="pool YT_1lb v SPD"
 /note="Organ: breast; Vector: pZero-1; Site_1: SphI;

Query Match 19.0%; Score 488; DB 12; Length 566;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Site 2: Sph1; Ductal carcinoma in situ, high-grade, comedo
, from 41 yo female. Library constructed in the laboratory
of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."

BASE COUNT 130 a 186 c 157 g 124 t
ORIGIN

Query Match 18.7%; Score 480; DB 9; Length 597;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 530; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 901 GCGCTCACTTCCCTCACTCCAGAGCCCTGAGACATTAATCTGAGCTGGAGATAC 960
Db 37 GCGCTCACTTCCCTCACTCCAGAGCCCTGAGACATTAATCTGAGCTGGAGATAC 96
QY 961 ATCTGCTCTACTCAAGAGCCCTGCTGCTGCAAGAGGCTGGCCCTCCCTGGCAG 1020
Db 97 ATCTGCTCTACTCAAGAGCCCTGCTGCTGCAAGAGGCTGGCCCTCCCTGGCAG 156
QY 1021 GATATACCCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 157 GATATACCCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 216
QY 1081 TCCCT 1140
Db 217 TCCCT 276
QY 1141 GAGTCCCTCACTTCTATCATGAGCTGATGAGAGGCTGCTCTTGTGATGCTTAC 1200
Db 277 GAGTCCCTCACTTCTATCATGAGCTGATGAGAGGCTGCTCTTGTGATGCTTAC 336
QY 1201 GCCCAAG 1260
Db 337 GCCCAAG 396
QY 1261 CTTGGGAG 1320
Db 397 CTTGGGAG 456
QY 1321 ATCTAGAGTCCCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Db 457 ATCTAGAGTCCCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 516
QY 1381 TCTTTCACTGAGTCCCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1440
Db 517 TCTTTCACTGAGTCCCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 576

RESULT 14

LOCUS AL844307 614 bp mRNA linear EST 30-JUL-2002
DEFINITION AL844307 pool_AK_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
ACCESSION AL844307
VERSION AL844307.1 GI:22019089
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 614)
Aashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and
Sheridan, E.

REFERENCE Homo sapiens EST sequence
JOURNAL Unpublished (2002)
COMMENT Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name: scd10816.14136A
Homo sapiens EST sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA library
resources. This sequence was obtained from a PCR product generated

from a pool of up to 100,000 cDNA clones derived from
pool_AK_11b_v_SPD cDNA library. Further information can be found at
<http://www.sanger.ac.uk/Teams/Team69/>.

FEATURES
source
1. 614
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_11b="pool_AK_11b_v_SPD"
/note="Organ: breast; Vector: pZE0-1; Site_1: Sph1;
Site_2: Sph1; Ductal carcinoma in situ, high-grade, comedo
, from 41 yo female. Library constructed in the laboratory
of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."

BASE COUNT 134 a 188 c 164 g 128 t
ORIGIN

Query Match 18.3%; Score 469; DB 9; Length 614;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 569; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 925 GCGCTGAGACATTAATCTGAGCTGGAGATGATGATGCTGCTGCTGCTGCTGCTG 984
Db 44 GCGCTGAGACATTAATCTGAGCTGGAGATGATGATGCTGCTGCTGCTGCTGCTG 103
QY 985 TGTGCTCTGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1044
Db 104 TGTGCTCTGAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 163
QY 1045 CAGAGACACACTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1104
Db 164 CAGAGACACACTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 223
QY 1105 ACAG 1164
Db 224 ACAG 283
QY 1165 CTGATGAG 1224
Db 284 CTGATGAG 343
QY 1225 AACCAAGGCTGACACCTTAAGACCTTAAGACCTTAAGACCTTAAGACCTTA 1284
Db 344 AACCAAGGCTGACACCTTAAGACCTTAAGACCTTAAGACCTTAAGACCTTA 403
QY 1285 GTGACTCAG 1344
Db 404 GTGACTCAG 463
QY 1345 GCTCTTCT 1404
Db 464 GCTCTTCT 523
QY 1405 TGGACCTCTAGTGCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1464
Db 524 TGGACCTCTAGTGCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
QY 1465 TAAGCTCTGAG 1495
Db 584 TAAGCTCTGAG 614

RESULT 15

LOCUS AL844310 611 bp mRNA linear EST 30-JUL-2002
DEFINITION AL844310 pool_FLU_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
ACCESSION AL844310
VERSION AL844310.1 GI:22019092
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 611)

AUTHORS Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and Sheridan, E.

TITLE Homo sapiens EST sequence

JOURNAL Unpublished (2002)

COMMENT Contact: The Sanger Centre

The Sanger Centre

Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK

Email: humquerry@sanger.ac.uk

Sanger Centre name: sccid10817.4004898

Homo sapiens EST sequence. This sequence was generated as part of the Wellcome Trust Sanger Institute program to identify and annotate genes in the human genome. Incomplete or unconfirmed genes are experimentally analysed using a variety of cDNA library resources. This sequence was obtained from a PCR product generated from a pool of up to 100,000 cDNA clones derived from pool FLU 11b v SPC cDNA library. Further information can be found at <http://www.sanger.ac.uk/Team/Team69/>.

FEATURES

Source

1. 611

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="20"

/clone_lib="pool FLU 11b v SPC"

/note="Organ: breast; Vector: pZERO-1; Site 1: SphI; Site 2: SphI; Ductal carcinoma in situ, high grade, comedo, from 41 yo female. Library constructed in the laboratory of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."

BASE COUNT 132 a 157 c 173 g 149 t

ORIGIN

Query Match 17.7%; Score 454; DB 9; Length 611;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 504; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1095 TGAAGTGGCCACAGGGAGAGTCTTCTCACTGAGAGGCTCCCGAGTCCCTCAAGCTT 1154

577 TGAAGTGGCCACAGGGAGAGTCTTCTCACTGAGAGGCTCCCGAGTCCCTCAAGCTT 518

1155 CTACATCAAGCTGGAATGACGAGGCTGTCTTTGATGATGCTTGAAGGCGCAAGAGAGG 1214

517 CTACATCAAGCTGGAATGACGAGGCTGTCTTTGATGATGCTTGAAGGCGCAAGAGAGG 458

1215 CCAAAAGGAAACCAAGGCTGCAACCTAGAAACCCCAATTCAGCTTCTGGGCAACCCAG 1274

457 CCAAAAGGAAACCAAGGCTGCAACCTAGAAACCCCAATTCAGCTTCTGGGCAACCCAG 398

1275 AGCAAGGCTGTGACTCAGGAGGAGGAGGAGGAGCAAGAGGTCATCTAGGGTCCAC 1334

397 AGCAAGGCTGTGACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 338

1335 CTGTACCTTCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1394

337 CTGTACCTTCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 278

1395 TGATCCCACTGCACTCTAGTGCAGAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1454

277 TGATCCCACTGCACTCTAGTGCAGAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 218

1455 AAAAAGAAATTAAGCTCTCTGGGGGCTTGAACCTAGTGAATTTGAGTTTGGGTTTCC 1514

217 AAAAAGAAATTAAGCTCTCTGGGGGCTTGAACCTAGTGAATTTGAGTTTGGGTTTCC 158

1515 AGTACCATCTGATGCTCTGCTGTTGAGCCCATTTCTACATCCCACTTAACAGGAG 1574

157 AGTACCATCTGATGCTCTGCTGTTGAGCCCATTTCTACATCCCACTTAACAGGAG 98

1575 CCAACCCAAAGGTAAACACACC 1599

97 CCAACCCAAAGGTAAACACACC 73

RESULT 16
BF510664/c

LOCUS BF510664 451 bp mRNA linear EST 06-DEC-2000

DEFINITION UI-H-B14-acf-b-01-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone

IMAGE:3084601.3', mRNA sequence.

ACCESSION BF510664

VERSION BF510664.1 GI:11593962

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (base 1 to 451)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. cDNA library preparation: M.B. Soares Lab Clone distribution:

NCI-CGAP clone distribution information can be found through the

I.M.A.G.E. Consortium/ILNL at:

www-bio.lnl.gov/bihrp/image/image.html

Seq primer: M3 Forward

FEATURES

Source

1. 451

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3084601"

/clone_lib="NCI CGAP Sub8"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pRT3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub8

is a subcloned library derived from NCI CGAP Sub5. The

NCI CGAP Sub8 library had 2.5 million recombinants. A

single-stranded DNA preparation of NCI CGAP Sub5 was used

as a tracer in a subtractive hybridization with a driver

clone Ids 2732833-2737415, 3068040-3069191, 25% of the

(IMAGE clone Ids 2723592-2729326; 25% of the driver

population), NCI CGAP Sub6 (pool AIF-AU, IMAGE Ids

2728969-2733190; 25% of the driver population), and

NCI CGAP Sub7 (IMAGE Ids 3069192-3072238, 3081864-3084550

; 25% of the driver population). Subtraction was

performed as previously described [Bonaldi, Lennon &

Soares (1996): Normalization and Subtraction: Two

Approaches To Facilitate Gene Discovery. Genome Research

6, 791-806.

TAG LIB=NCI CGAP Col10

TAG TISSUE=colon

TAG SEO=AAACG

BASE COUNT 97 a 110 c 115 g 129 t

Query Match 17.2%; Score 441; DB 12; Length 451;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2121 GGCACCCAGCTGCTCAGATCTATTCTATTGTTGGCTTACATCCCTACACACA 2180

441 GGCACCCAGCTGCTCAGATCTATTCTATTGTTGGCTTACATCCCTACACACA 382

2181 CTGGCTTGCATCTTTGGCCGAATTAATAATTAACCTCTTAAGTTCAGCACTGCA 2240

381 CTGGCTTGCATCTTTGGCCGAATTAATAATAATTAACCTCTTAAGTTCAGCACTGCA 322

2241 GTGAGGCGAGGCACTCACTGCTGGGCGAGGCGATCAGAGTCTCAAGCCCTCTCCA 2300

321 GTGAGGCGAGGCACTCACTGCTGGGCGAGGCGATCAGAGTCTCAAGCCCTCTCTCA 262

QY 2301 CAATGCCAAGAGGAGACCAAGCTACACCAATCCAGCCCTTGATTTCTCTGCTGCT 2260
 DB 261 CAATGCCAAGAGGAGACCAAGCTACACCAATCCAGCCCTTGATTTCTCTGCTGCT 202
 QY 2361 CCATTAACAGAAAGAGGTCTGCTGATCCGCTTAAGGATCGAGAGAGAGAAAGAGG 2420
 DB 201 CCATTAACAGAAAGAGGTCTGCTGATCCGCTTAAGGATCGAGAGAGAGAAAGAGG 142
 QY 2421 ATGGGGTGGAGGACCCCTCCAGTCTCTCACTGCTTCCCAAGCTACAGGTGGGGTGG 2480
 DB 141 ATGGGGTGGAGGACCCCTCCAGTCTCTCACTGCTTCCCAAGCTACAGGTGGGGTGG 82
 QY 2481 GAAAGCTTTATCAGTATCATCAACAGTTCTCAATTAAAGATTGATTTATCACTA 2540
 DB 81 GAAAGCTTTATCAGTATCATCAACAGTTCTCAATTAAAGATTGATTTATCACTA 22
 QY 2541 TGTGAAAAAAAAAAAAAAAA 2561
 DB 21 TGTGAAAAAAAAAAAAAAAA 1

RESULT 17
 BGI78487 778 bp mRNA linear EST 06-FEB-2001
 LOCUS 602328305F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4429856 5',
 DEFINITION mRNA sequence.
 ACCESSION BGI78487
 VERSION BGI78487.1 GI:12685190
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 778)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@ps-remail.nih.gov
 Tissue Procurement: DCTP/DRP
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM10182 row: 1 column: 01
 High quality sequence stop: 657.
 Location/Qualifiers
 1..778
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4429856"
 /clone_id="NIH_MGC_91"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: prostate; Vector: PCMV-SPORT6; Site 1: NciI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.4 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: This is a NIH MGC Library."

BASE COUNT 179 a 224 c 230 g 145 t
 ORIGIN

Query Match 17.0%; Score 436; DB 12; Length 778;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 606; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 79 CTTCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 138
 DB 26 CTTCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 85
 QY 139 ATGGGAGCTATCATCATCCCTGGGTGTAACAACTGTATCGACAGACAGTCTGAGCTA 198

DB 86 ATGGGAGCTATCATCATCCCTGGGTGTAACAACTGTATCGACAGACAGTCTGAGCTA 145
 QY 199 CCCAAACCAACCTAGCCTCTCTGAAAGATCTCTCCAGGCTGAGAGATTTCTGGGCTG 258
 DB 146 CCCAAACCAACCTAGCCTCTCTGAAAGATCTCTCCAGGCTGAGAGATTTCTGGGCTG 205
 QY 259 CTTAGGACCAAGGACACTGGCAGACTCTCCAGAGAGGCCCCCAAGCCTTAACCTGTCAG 318
 DB 206 CTTAGGACCAAGGACACTGGCAGACTCTCCAGAGAGGCCCCCAAGCCTTAACCTGTCAG 265
 QY 319 CCAAGCATGCTCTCAGCAGAGCTGCTCTCCAGCCTTTATGATCAACCAATTTTCC 378
 DB 266 CCAAGCATGCTCTCAGCAGAGCTGCTCTCCAGCCTTTATGATCAACCAATTTTCC 325
 QY 379 TCGATGATGCTCTCTGAGTCTCTGAGAGAACTTGGGAAAGTCTGCCAGAGAA 438
 DB 326 TCGATGATGCTCTCTGAGTCTCTGAGAGAACTTGGGAAAGTCTGCCAGAGAA 385
 QY 439 AAATCTTCCCAAGCCCAAGCTTGAAGTCTCTGTCCTCAAGCCAGGACCTTGACCATG 498
 DB 386 AAATCTTCCCAAGCCCAAGCTTGAAGTCTCTGTCCTCAAGCCAGGACCTTGACCATG 444
 QY 499 GAAGCAGAGAGAGAGAGGACAGCCGAGGCTCTGGGAGGTTCCCGGAGTGGCCG 558
 DB 445 GAAGCAGAGAGAGAGAGGACAGCCGAGGCTCTGGGAGGTTCCCGGAGTGGCCG 504
 QY 559 GCCGAGCTGCTGCTGAGACTCTGGGAGGACCATTAACCATGCTCTGAGAGTGAAGTGG 618
 DB 505 GCCGAGCTGCTGCTGAGACTCTGGGAGGACCATTAACCATGCTCTGAGAGTGAAGTGG 564
 QY 619 TGAGAGCTGCTGCTGAGAGTCTGAGGACAGAGATATTAATCCCAAGGCTCAAGTGGCC 678
 DB 565 TGAGAGCTGCTGCTGAGAGTCTGAGGACAGAGATATTAATCCCAAGGCTCAAGTGGCC 624
 QY 679 AAAGTCTC 686
 DB 625 AAAGTCTC 632

RESULT 18
 A1476149/c 409 bp mRNA linear EST 14-APR-1999
 LOCUS tnc6212.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2174158 3'
 DEFINITION similar to contains element MER22 repetitive element ; mRNA
 sequence.
 ACCESSION A1476149
 VERSION A1476149.1 GI:4329183
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap/
 1 (bases 1 to 409)
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@ps-remail.nih.gov
 Life Technologies catalog #: 11547-015
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.llnl.gov/bbrp/image/image.html
 Insert length: 2148 Srd Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 409.
 Location/Qualifiers
 1..409
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2174158"

FEATURES
 source

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/clone_lib="NCI_CGAP_Lym12"
/tissue_type="lymphoma, follicular mixed small and large
cell"
/lab_host="DH10B"
/note="Organ: lymph node; Vector: PCMV-SPORT6; Site 1:
Sali; Site 2: Nci; Cloned unidirectionally. Primer:
Oligo dt. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"

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BASE COUNT      94 a      100 c      109 g      106 t
ORIGIN
Query Match      15.9%; Score 409; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2127 CAGCCATCTCTCAGATCTCTATTTTCACTTTTGTGCTTACCACTCCCTCAGACACCTGGCC 2186
Db 409 CAGCCATCTCTCAGATCTCTATTTTGTGCTTACCACTCCCTCAGACACCTGGCC 350
Qy 2187 TTGCCATCTTGTGGCCGAAATATAACACCTTTAAGTCTAGACACCTGAGTGAAG 2246
Db 349 TTGCCATCTTGTGGCCGAAATATAACACCTTTAAGTCTAGACACCTGAGTGAAG 290
Qy 2247 CCAGGACCTCAGTGTGGGCGAGGCGCATCAGAGGTCTAGACCCCTCTCCACATGC 2306
Db 289 CCAGGACCTCAGTGTGGGCGAGGCGCATCAGAGGTCTAGACCCCTCTCCACATGC 230
Qy 2307 CAAGAAGAGACACACAGCCTTACCAAAATCCAGCCCTTGTTCCTGCTCCATTA 2366
Db 229 CAAGAAGAGACACACAGCCTTACCAAAATCCAGCCCTTGTTCCTGCTCCATTA 170
Qy 2367 ACAGAAAGAGGTCTGTGATTCGGCTAAGAGGATAGAGAGAGAGAGAGAGAGAGAG 2426
Db 169 ACAGAAAGAGGTCTGTGATTCGGCTAAGAGGATAGAGAGAGAGAGAGAGAGAGAG 110
Qy 2427 TGGAGAGACCCCTCCAGTGTCTCTCACTGCTTCCAGCTACAGTGGGTGGAGAG 2486
Db 109 TGGAGAGACCCCTCCAGTGTCTCTCACTGCTTCCAGCTACAGTGGGTGGAGAG 50
Qy 2487 CTTTATCAGATATCATCAAGATTTCTCAATTAAGATTGATTATTC 2535
Db 49 CTTTATCAGATATCATCAAGATTTCTCAATTAAGATTGATTATTC 1

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RESULT 19      397 bp      mRNA      linear      EST 16-OCT-2000
BF057252/c      7k18a03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:344389 3',
DEFINITION      mRNA sequence.
ACCESSION      BF057252
VERSION        BF057252.1 GI:10811148
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens

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REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE      1 (bases 1 to 397)
JOURNAL      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

```

```

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLML, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco.

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FEATURES
source      Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:344389"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pRT3D-Pac (pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
58 circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

```

```

BASE COUNT      88 a      100 c      109 g      109 t
ORIGIN
Query Match      15.5%; Score 397; DB 12; Length 397;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 2154 TTTTGTGCTTACCACTTCCCTAGACACCTGCTTGTGCTGCGAATATAAAT 2213
Db 397 TTTTGTGCTTACCACTTCCCTAGACACCTGCTTGTGCTGCGAATATAAAT 338
Qy 2214 AACACCTCTTAAGCTTACGACACCTGAGGCGAGGACCTGAGTGGGCGAGGGG 2273
Db 337 AACACCTCTTAAGCTTACGACACCTGAGGCGAGGACCTGAGTGGGCGAGGGG 278
Qy 2274 ATCAGAGGTGCTTAACCTCTCTTCCAAATGCGAAGAGAGACACAGCTTACCA 2333
Db 277 ATCAGAGGTGCTTAACCTCTCTTCCAAATGCGAAGAGAGACACAGCTTACCA 218
Qy 2334 ATCCAGCCCTTGAATTTCCCTGCTCTCTCAATAAGAGAGTGTGATCCGCTA 2393
Db 217 ATCCAGCCCTTGAATTTCCCTGCTCTCTCAATAAGAGAGTGTGATCCGCTA 158
Qy 2394 AGGATTCAGGAGAGAGAGAGAGAGAGTGGGTGGAGAGACCCCTCCAGTCTCTTA 2453
Db 157 AGGATTCAGGAGAGAGAGAGAGAGAGTGGGTGGAGAGACCCCTCCAGTCTCTTA 98
Qy 2454 CTGATTCCTCAAGTACAGTGTGGGTGGAGAGCTTTATCAGATATCATCAAGATTCT 2513
Db 97 CTGATTCCTCAAGTACAGTGTGGGTGGAGAGCTTTATCAGATATCATCAAGATTCT 38
Qy 2514 CAATTAAAGATTGATTATTTCAAGTATGCAAAAA 2550
Db 37 CAATTAAAGATTGATTATTTCAAGTATGCAAAAA 1

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RESULT 20      397 bp      mRNA      linear      EST 16-OCT-2000
BF062179/c      7k13e03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3481060 3',
DEFINITION      mRNA sequence.
ACCESSION      BF062179
VERSION        BF062179.1 GI:10821089
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens

```

```

REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE      1 (bases 1 to 397)
JOURNAL      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

```

R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bernaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
 Seq primer: -400P from Gibco.

FEATURES

source

1. .397
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3481060"
 /clone_lib="NCI CGAP GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bernaldo."

BASE COUNT

88 a 100 c 100 g 109 t

ORIGIN

Query Match 15.5%; Score 397; DB 12; Length 397;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2154 TTTTGGCTTACCATTCCTTACGACACTGCGCTTGCATTTGTGGCCGATAAATAAT 2213
 DB 397 TTTTGGCTTACCATTCCTTACGACACTGCGCTTGCATTTGTGGCCGATAAATAAT 338
 QY 2214 AACACCTTTAAGCTAGACACTGAGTAGAGGCGACCTGAGTGGGAGGCGC 2273
 DB 337 AACACCTTTAAGCTAGACACTGAGTAGAGGCGACCTGAGTGGGAGGCGC 278
 QY 2274 ATCAGAGGCTTAAAGCCCTCTCTCCCAATGCGAAGCGAGACAGCCTTACACCA 2333
 DB 277 ATCAGAGGCTTAAAGCCCTCTCTCTCCCAATGCGAAGCGAGACAGCCTTACACCA 218
 QY 2334 ATCCAGCCCTTGAATTCCTCTCTCTCATTAACGAAGAGTCTGTGATCCGCTA 2393
 DB 217 ATCCAGCCCTTGAATTCCTCTCTCTCATTAACGAAGAGTCTGTGATCCGCTA 158
 QY 2394 AGGATCAGGAG 2453
 DB 157 AGGATCAGGAG 98
 QY 2454 CTGGTTCCTCAAGCTACAGGTGGGGTGGAAAGGCTTTATCAGATATCAACAGATTCT 2513
 DB 97 CTGGTTCCTCAAGCTACAGGTGGGGTGGAAAGGCTTTATCAGATATCAACAGATTCT 38
 QY 2514 CAATTAAGATTTGATTTATTCAGTATGGAATAA 2550
 DB 37 CAATTAAGATTTGATTTATTCAGTATGGAATAA 1

RESULT 21

BO053486 878 bp mRNA linear EST 29-MAR-2002
 LOCUS AGENCOURT 6822017 NIH_MGC_106 Homo sapiens CDNA IMAGE:5935253
 DEFINITION 5', mRNA Sequence.
 ACCESSION BO053486
 VERSION BO053486.1 GI:19812826
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 878)
 NIH-MGC http://mgs.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs-rc@mail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DMS/NCI
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM2122 row: 1 column: 06
 High quality sequence stop: 394.

FEATURES

source

1. .878
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5935253"
 /clone_lib="NIH MGC 106"
 /tissue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: blood; Vector: pDRB1; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT

201 a 253 c 233 g 190 t 1 others

ORIGIN

Query Match 15.2%; Score 390; DB 14; Length 878;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 196 CTACCCAAACCAACTAGCTCTCCGGAAGATCTCCCAAGGCTGAGAGATTCTGGG 255
 DB 54 CTACCCAAACCAACTAGCTCTCCGGAAGATCTCCCAAGGCTGAGAGATTCTGGG 113
 QY 256 TGTCTTAGAGCAAGAGCACTGGCAGACTTCCAGAGAGGCCCCCAAGCCTTAACCTGTC 315
 DB 114 TGTCTTAGAGCAAGAGCACTGGCAGACTTCCAGAGAGGCCCCCAAGCCTTAACCTGTC 173
 QY 316 CAGCAGACATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTGTATGACAAACAATT 375
 DB 174 CAGCAGACATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTGTATGACAAACAATT 233
 QY 376 CCTCGATGATGTGCTTCTGAGTCTCTGCTGAGAGAACTATGAGAGTCTCCAGAGAG 435
 DB 234 CCTCGATGATGTGCTTCTGAGTCTCTGCTGAGAGAACTATGAGAGTCTCCAGAGAG 293
 QY 436 AGAAATCTCTGCAAGCCCAAGCTTGAATCTCTGCTCAAGGCGCAGAGGAGCTGTAGCC 495
 DB 294 AGAAATCTCTGCAAGCCCAAGCTTGAATCTCTGCTCAAGGCGCAGAGGAGCTGTAGCC 353
 QY 496 ATGGAAGCAG 555
 DB 354 ATGGAAGCAG 413
 QY 556 CCGGCGAGAGCTGCTGAGAGCTGGGAGAGCATTGACATCGCTCTGAGAGATGAGAG 615
 DB 414 CCGGCGAGAGCTGCTGAGAGCTGGGAGAGCATTGACATCGCTCTGAGAGATGAGAG 473
 QY 616 TGGTGAACGGTGTCTGTCTGAA 636
 DB 474 TGGTGAACGGTGTCTGTCTGAA 494

RESULT 22

A1476150/c 301 bp mRNA linear EST 09-MAR-1999
 LOCUS tnc2f01.x1 NCI_CGAP_Lym12 Homo sapiens CDNA clone IMAGE:2174137 3',
 DEFINITION mRNA sequence.
 ACCESSION A1476150
 VERSION A1476150.1 GI:4329184
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 301)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-remail.nih.gov
 Life Technologies catalog #: 11547-015
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seg primer: -40UP from Gibco
 High quality sequence stop: 283.
 Location/Qualifiers
 1..301
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2174137"
 /clone_lib="NCI CGAP Lym12"
 /tissue_type="lymphoma, follicular mixed small and large
 cell"
 /lab_host="DH10B"
 /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
 Salt; Site_2: NotI; Cloned unidirectionally. Primer:
 Oligo dt. Average insert size 1.25 kb. Life Technologies
 catalog #: 11547-015"
 BASE COUNT 61 a 84 c 77 g 79 t
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2235 ACTGACGTGAGCCAGCACTCAGTCTGGCGAGGGGATCAGAAGTGTCTAAGCCCTC 2294
 Db 301 ACTGACGTGAGCCAGCACTCAGTCTGGCGAGGGGATCAGAAGTGTCTAAGCCCTC 242
 QY 2295 TCTCCAAATGCCAAGCGAGACACAGCTTAACCAATCCAGCCCTTGAATTCCTG 2354
 Db 241 TCTCCAAATGCCAAGCGAGACACAGCTTAACCAATCCAGCCCTTGAATTCCTG 182
 QY 2355 CTGCTCCATTAACAGAAAGAGTCTGCTGATCCGTAAGGATCAGAGAGAGAA 2414
 Db 181 CTGCTCCATTAACAGAAAGAGTCTGCTGATCCGTAAGGATCAGAGAGAGAA 122
 QY 2415 AAGAGGATGGGTGGAGGACCCCTCAATGCTCTACTGTCCCAAGCTTCAAGGTG 2474
 Db 121 AAGAGGATGGGTGGAGGACCCCTCAATGCTCTACTGTCCCAAGCTTCAAGGTG 62
 QY 2475 GGGTGGAAAGCTTTATCAGGTATCAACAGGTCTCAATTAAGATTGATTATT 2534
 Db 61 GGGTGGAAAGCTTTATCAGGTATCAACAGGTCTCAATTAAGATTGATTATT 2
 QY 2535 C 2535
 Db 1 C 1
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 BF059756/c 397 bp mRNA linear EST 16-OCT-2000
 LOCUS BF059756

DEFINITION 7k65h11.x1 NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:3480452 3',
 mRNA sequence.
 ACCESSION BF059756
 VERSION BF059756.1 GI:10813652
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 397)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL, send email to:
 info@image.llnl.gov
 Seg primer: -40UP from Gibco.
 Location/Qualifiers
 1..397
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3480452"
 /clone_lib="NCI CGAP GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: p773D-Pac (pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
 from the normalized library NCI CGAP GC4 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (cloneids
 157096-1258531, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 89 a 99 c 110 t
 ORIGIN
 Query Match 11.5%; Score 295; DB 12; Length 397;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2154 TTTGTGGCTTACCATTCCTAGACACCTGCTGCAATCTTGTGGCGAATAAATAAT 2213
 Db 397 TTTGTGGCTTACCATTCCTAGACACCTGCTGCAATCTTGTGGCGAATAAATAAT 338
 QY 2214 AACACCTTAACTAGACACCTGAGGAGGACCTGAGTGGGCGAGGGG 2273
 Db 337 AACACCTTAACTAGACACCTGAGGAGGACCTGAGTGGGCGAGGGG 278
 QY 2274 ATCAGAAAGTGTCTAAGCCCTCTTCCAAATGCCAAGCGAGACCAAGCTTACCA 2333
 Db 277 ATCAGAAAGTGTCTAAGCCCTCTTCCAAATGCCAAGCGAGACCAAGCTTACCA 218
 QY 2334 ATCCAGCCCTTGAATTTCCCTGCTGCTCCATTAACAGAAAGAGTTTGTGATCCGCTA 2393
 Db 217 ATCCAGCCCTTGAATTTCCCTGCTGCTCCATTAACAGAAAGAGTTTGTGATCCGCTA 158
 QY 2394 AAGGATCAGGAG 2453
 Db 157 AAGGATCAGGAG 98
 QY 2454 CTGATCCCAAGCTACAGGTGGGTGGAAAGGCTTTATCAGGTATCAACAGGTCT 2513
 Db 97 CTGATCCCAAGCTACAGGTGGGTGGAAAGGCTTTATCAGGTATCAACAGGTCT 38

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QY 2514 CAATTAAAGATTGTATTATTCACGATGTGAAAAA 2550
      |||||
Db 37 CAATTAAAGATTGTATTATTCACGATGTGAAAAA 1
```

[illegible]

REFERENCE 1 (bases 1 to 522)

Plate: L1AM10302 row: 1 column: 02
High quality sequence stop: 522.
location/Qualifiers

BASE COUNT	126 a	146 c	121 g	129 t
ORIGIN				

Accession	Sequence	Position
Oy	GTGATTTTCAGAAAATCTACAAAGCTCTGTTGAGCAACACCATCTCTCAGAAAGTAGA	1676
Dp	1 GTGATTTTCAGAAAATCTACAAAGCTCTGTTGAGCAACACCATCTCTCAGAAAGTAGA	60
Oy	1677 CTGTGGCCCTGAAGGGGAAAGGACGTGATGATGCTTACCGTAGACGACATCTTGG	1736
Dp	61 CTGTGGCCCTGAAGGGGAAAGGACGTGATGATGCTTACCGTAGACGACATCTTGG	120
Oy	1737 ATGGCTCAGGCTCTATGTGACCTCCAGACAAAGAAAGAACTTGGACAGCTTAGGTC	1796
Dp	121 ATGGCTCAGGCTCTATGTGACCTCCAGACAAAGAAAGAAAGCTTGGACAGCTTAGGTC	180
Oy	1797 TCAAATGTCCTCCCATTTGAGACAAACAGCCCAAGCTCTTTTCTTTTCTTTTGTGACGAG	1856
Dp	181 TCAAATGTCCTCCCATTTGAGACAAACAGCCCAAGCTCTTTTCTTTTCTTTTGTGACGAG	239
Oy	1857 TCTTGCCCTGTGCCCATGCTGGAGTGCATATGACATCTCAGCTCATCTGCAACTCCA	1916
Dp	240 TCTTGCCCTGTGCCCATGCTGGAGTGCATATGACATCTCAGCTCATCTGCAACTCCA	299

QY	1917	TCTCTGGATTCAAAACAATTCTCTGCTCAAGCTCAGAAATGCTGGGATTAACAGCGT	1976
Db	300	TCTCTGGATTCAAAACAATTCTCTGCTCAAGCTCAGAAATGCTGGGATTAACAGCGT	359
QY	1977	ACAGCAGATGCTGCTAATTT	1999
Db	360	ACAGCAGATGCTGCTAATTT	382

RESULT	25
ALB44309	
LOCUS	606 bp mRNA linear EST 30-JUL-2002
DEFINITION	ALB44309 pool_FIU_1lb_v_SPC Homo sapiens cDNA, mRNA sequence.
ACCESSION	ALB44309
VERSION	ALB44309.1 GI:22019091
KEYWORDS	EST,
SOURCE	Homo sapiens
ORGANISM	Human.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 606)	Ashcroft, K., Bethel, G., Bye, J. M., Howell, G. R., Huckle, E. J. and Sheridan, E.	Homo sapiens EST sequence	Unpublished (2002)	
		Contact: The Sanger Centre		The Sanger Centre

Sanger Centre name : sc00017.154358
Homo sapiens EST sequence.
The Wellcome Trust Sanger Institute program to identify and annotate genes in the human genome. Incomplete or unconfirmed genes are experimentally analysed using a variety of cDNA library resources. This sequence was obtained from a PCR product generated from a pool of up to 100,000 cDNA clones derived from pool FLU 11b v SPC cDNA library. Further information can be found at <http://www.sanger.ac.uk/Teams/team69/location/analysts>

BASE COUNT	138 a	186 c	154 g	125 t	3 others
ORIGIN					

Oy	925	GGCTGGGAGACCATTAATCTGAGCTGGGGATACATCTGCTCTACCAAGAGCC	984
Db	46	GGCTGGGAGACCATTAATCTGAGCTGGGGATACATCTGCTCTACCAAGAGCC	105
Oy	985	TGTGTCTCGAAGAGGCTGGCGCCGCTCCTGGGAAGATATCCCTACCTGTGACTG	1044
Db	106	TGTGTCTCGAAGAGGCTGGCGCCGCTCCTGGGAAGATATCCCTACCTGTGACTG	165
Oy	1045	CAGAAGACACCACTGAAAGAGCTGAGACAGCTCCCTCTGTGTAAGCTCC	1104
Db	166	CAGAAGACACCACTGAAAGAGCTGAGACAGCTCCCTCTGTGTAAGCTCC	225
Oy	1105	AACAGGGAGAGAGCTCTCTCAGTGAAGGGTCTCCGGGAGATCCCTACGTTCTACATGAC	1164
Db	226	AACAGGGAGAGAGCTCTCTCAGTGAAGGGTCTCCGGGAGATCCCTACGTTCTACATGAC	285
Oy	1165	CTGAATGACAGGCTGTCTCTTTGGATGATGCTTAGGCCCAAGAGAGGCCCAAAAGGA	1224

QY 2281 GGTCCTAAGCCCTCTCTCCACCAATGCCAAGCGAGACCACAGCCTTACACCAAAATCCAGC 2340

RESULT 28					
AI002059/c					
LOCUS	AI002059	110 bp	mRNA	linear	EST 09-JUN-1996
DEFINITION	os757a07.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1613268 3'				

ACCESSION mRNA sequence.
 A1002059
 VERSION A1002059.1 GI:3202096
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 110)
 AUTHORS NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NC1-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/biopr/image/image.html
 Seq primer: -40ml3 fwd RT from Amersham.

FEATURES

source
 1. 110
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1613268"
 /clone_1ib="NC1 CGAP GC3"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from 3 pooled
 germ cell tumors, and was then prepared with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. Library is not normalized. Library was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 28 a 21 c 15 g 46 t
 ORIGIN

Query Match 3.5%; Score 90; DB 9; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2451 CTACTGGTCCCAAGCTACAGTGGGTGGGAAAGCTTTATCAGTATCATCAACAGGT 2510
 Db 110 CTACTGGTCCCAAGCTACAGTGGGTGGGAAAGCTTTATCAGTATCATCAACAGGT 51

QY 2511 TCTCAATTAAGATTGATTATTCAGTA 2540
 Db 50 TCTCAATTAAGATTGATTATTCAGTA 21

RESULT 29
 LOCUS AA309769 149 bp mRNA linear EST 19-APR-1997
 DEFINITION EST180699 Jurkat T-cells V Homo sapiens cDNA 5' end, mRNA sequence.
 ACCESSION AA309769
 VERSION AA309769.1 GI:1962171
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 149)
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulmer, R.A., Bult
 C.J., Lee, N.H., Kirschner, E.F., Weinstock, K.G., Gocayne, J.D., White
 O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wei, C., Claydon, R.A.,
 Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald,
 J.M., Fitzhugh, W.M., Fitchman, J.L., Geoghegan, N.S., Giordano, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M.,
 Kelley, J.C., Liu, L., Martiros, S.M., Merrick, J.M.,
 Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pellierino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Utecher, T.R., Weidman, J.F., Li, Y.,
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
 Dimke, D., Fang, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,
 Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
 Kunsch, C., Hungjun, J., Li, H., Weisner, P.S., Olsen, H., Raymond, L.,
 Wei, T.F., Wang, J., Xu, C., Yu, G., Ruden, S.M., Dillon, P.J., Fannon
 M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
 Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 9606280
 COMMENT Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423

Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse
 Location/Qualifiers

FEATURES
 source
 1. 149
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):155929"
 /db_xref="taxon:9606"
 /clone_1ib="Jurkat T-cells V"
 /cell_type="T-lymphocyte"
 /note="Vector: pBluescript SK-; Site 1: EcoRI, Site 2:
 XhoI"

BASE COUNT 38 a 46 c 36 g 27 t 2 others
 ORIGIN

Query Match 3.0%; Score 76; DB 9; Length 149;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 AAAAGGAAACCAAGCTGCACCTAGAACCCCAATTCAGCTCTGGGACCCAGAG 1276
 Db 74 AAAAGGAAACCAAGCTGCACCTAGAACCCCAATTCAGCTCTGGGACCCAGAG 133

QY 1277 GCAAGGCTGTGCACTC 1292
 Db 134 GCAAGGCTGTGCACTC 149

RESULT 30
 LOCUS AQ341462/c 489 bp DNA linear GSS 06-MAY-1999
 DEFINITION RPII11-11111.TV RPII-11 Homo sapiens genomic clone RPII-11-11111,
 DNA sequence.

ACCESSION AQ341462
 VERSION AQ341462.1 GI:416358
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 489)
 AUTHORS Zhao, S., Adams, M.D., Niernan, W., Malek, J., de Jong, P. and Venter
 J.C.
 TITLE Use of BAC End Sequences from Library RPII-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other GSSs: RPII11-11111.TV
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208

Email: hbe@igr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.igr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES

source location/Qualifiers
1..489
/organism="Homo sapiens"
/db_xref="GB:7542514"
/db_xref="taxon:9606"
/clone="RPCI-11-111111"
/clone_11b="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT 140 a 100 c 102 g 147 t
ORIGIN

Query Match 2.9%; Score 74; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2035 TTGGCCAGGCTGTGTGGAACCTCGACCTGATGATCCACCACTTGCCCTCCCAA 2094
DB 372 TTGGCCAGGCTGTGTGGAACCTCGACCTGATGATCCACCACTTGCCCTCCCAA 313
QY 2095 GTGCTGGGATTACA 2108
DB 312 GTGCTGGGATTACA 299

RESULT 31
LOCUS AQ431946 534 bp DNA linear GSS 31-MAR-1999
DEFINITION HS_5065_A2_P08_T7A RPCI-11 Human Male BAC Library Homo sapiens
ACCESSION AQ431946
VERSION AQ431946.1 GI:4542281
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Mahaitas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahaitas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu

Plate: 641 row: K column: 16
Seq primer: T7
Class: BAC ends
High quality sequence stop: 534.
Location/Qualifiers
1..534

FEATURES

source location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate:641 Col:16 Row=K"
/clone_11b="RPCI-11 Human Male BAC Library"
/sex="Male"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
BASE COUNT 144 a 105 c 119 g 155 t 11 others
ORIGIN

Query Match 2.9%; Score 74; DB 17; Length 534;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2035 TTGGCCAGGCTGTGTGGAACCTCGACCTGATGATCCACCACTTGCCCTCCCAA 2094
DB 401 TTGGCCAGGCTGTGTGGAACCTCGACCTGATGATCCACCACTTGCCCTCCCAA 342
QY 2095 GTGCTGGGATTACA 2108
DB 341 GTGCTGGGATTACA 328

RESULT 32
LOCUS BG943550/c 572 bp mRNA linear EST 11-JUN-2001
DEFINITION ax39b11.x1 Proliferating Human Erythroid Cells (LCB:ax library)
ACCESSION BG943550
VERSION BG943550.1 GI:14342922
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Gublin, A.N., Njoroge, J.M., Bouffard, G.G. and Miller, J.L.
TITLE Gene expression in proliferating human erythroid cells
JOURNAL Genomics 59 (2), 168-177 (1999)
MEDLINE 99339881
COMMENT Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD 20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jlm7@nih.gov

DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).
Plate: 39 row: D column: 11
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1..572

FEATURES

source location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ax39b11"
/clone_11b="Proliferating Human Erythroid Cells (LCB:ax library)"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"

```

BASE COUNT
ORIGIN
162 a 122 c 144 g 144 t
/dev stage="Progenitor; EBO responsive CD114++++"
/lab host="SOLR"
/node="Organ; blood; Vector: Lambda Zap II; Site 1: EcoRI
site 2: EcoRI; 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
cytometric separation after a 5-day culture period in the
presence of cell population using TRIO reagent. RNA (0.3
ug) was converted into double stranded cDNA using
Clontech's Capfinder cDNA Library Construction Kit
(Clontech) according to the manufacturer's protocol and
cloned into EcoRI digested Lambda Zap II vector
(Stratagene). The phage library was amplified once prior
to in vivo excision in SOLR cells. Individual colonies
were grown, and the cDNA inserts were sequenced in high
throughput (NIN intramural sequencing center
http://www.nisc.nih.gov/)."

```

Qy	2050	TCGAACCTCCGAGCTCAGGTATATCCACCACCTGGCTCCCAAGTCTGGGATTACG	2109
Db	375	TCGAACCTCCGAGCTCAGGTATATCCACCACCTGGCTCCCAAGTCTGGGATTACG	316
Qy	2110	GTCTGAGCCACGG	2122
Db	315	GTCTGAGCCACGG	303

Query Match 2.8%; Score 73; DB 13; Length 572;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT	33
AM247089	
LOCUS	503 bp mRNA linear EST 07-JAN-2000
DEFINITION	2822458.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822458 5'
ACCESSION	AM247089
VERSION	AM247089
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 503) NIH-MGC http://mgs.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS	Unpublished (1999)
JOURNAL	Other_ESTs: 2822458.3prime
COMMENT	

```

FEATURES
    source
        1. .503
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2822458"
            /clone_1ib="NIH_MGC 7"
            /tissue_type="small cell carcinoma"
            /cell_line="MGC3"
    Location/Qualifiers
        High quality sequence. stop: 454.
        Plate: LHC9 row: H column: 11
        http://www.genome.washington.edu
        PRRAD scores: PRRAD from University of Washington Genome Center. Vector
        titriming: cross match from University of Washington Genome Center
        PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
        Dirosophila Genome Project. University of Washington Genome Center
        http://www.genome.washington.edu

```

```

Query Match          2.8% Score 71; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy 2050 TCGAATCTCTGACTCTAGGTGATCCACCCACCTTGCGCTTCCCAAGTGTGGGATTACAG 2109
Db 199 TCGAATCTCTGAACTTCAGTATCCACCCACCTTGCGCTTCCCAAGTGTGGGATTACAG 258

Oy 2110 GTGTGAGCCAC 2120
Db 259 GTGTGAGCCAC 269

BASE COUNT      110 a      149 c      117 g      127 t,
ORIGIN
/lab host="DH10B (phage-resistant)"
/note="Organ: Lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGGACGAC(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the Laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

RESULT 34	BQ016908	637 bp	mRNA	linear	EST 17-JUN-2007
LOCUS	BQ016908				
DEFINITION	UI-H-DIC-auz-d-06-0-01.a1 NCI CCAP-D10 Homo sapiens cDNA clone IMAGE:5876309 3', mRNA sequence.				
ACCESSION	BQ016908				
VERSION	BQ016908.1	GI:19752185			
KEYWORDS	EST.				
SOURCE	human.				

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
1 (bases 1 to 637)
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Library Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/MLN at: <http://image.jim.gov>
The following repetitive elements were found in this cDNA
sequence: 14-143, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

```

FEATURES
Source
Location/Qualifiers
1..637
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5876309"
/clone_id="NCI CGAP D10"
/tissue_type="Lung Focal Fibrosis"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Lung; Vector: pTV73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; Not CGAP D10 is a cDNA library containing the following [isolate]: A pool of lung Focal Fibrosis. The library was constructed according to Bonald, Lennon and Soares, Genome Research, 6:791-806, 1996."
synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTV73-Pac vector. The oligonucleotide used to prime

```



```

ACCESSION      mRNA sequence.
VERSION        BE904397
KEYWORDS       BE904397.1 GI:10396608
SOURCE         EST.
ORGANISM       human.
               Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 737)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-remail.nih.gov
               Tissue Procurement: ATCC
               CDNA Library Preparation: Life Technologies, Inc.
               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LNL at:
               http://image.lnl.gov
               Plate: L1M9694 row: 1 column: 04
               High quality sequence stop: 673.
FEATURES
  source
    1..737
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:3898443"
    /clone_lib="NIH_MGC_70"
    /tissue_type="epitheloid carcinoma"
    /lab_host="DH10B (phage-resistant)"
    /note="Organ: Pancreas; Vector: pCMV-Sport6; Site 1: NotI;
    Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
    Average insert size 1.1 Kb. Library constructed by Life
    Technologies."
BASE COUNT      162 a 187 c 196 g 192 t
ORIGIN
Query Match      2.8%; Score 71; DB 12; Length 737;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2050 TCGAATCTCTGACCTGAGTATGATCCACCCCTTGCTCCAAAGTGTGGATTACG 2109
DB 216 TCGAATCTCTGACCTGAGTATGATCCACCCCTTGCTCCAAAGTGTGGATTACG 275
QY 2110 GTGTGAGCCAC 2120
DB 276 GTGTGAGCCAC 286

RESULT 38
BF664472      832 bp mRNA linear EST 21-DEC-2000
LOCUS         602146234F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4309876 5',
DEFINITION    mRNA sequence.
ACCESSION     BF664472
VERSION       BF664472.1 GI:11938277
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 832)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-remail.nih.gov
               Tissue Procurement: ATCC
               CDNA Library Preparation: Life Technologies, Inc.
               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LNL at:
               http://image.lnl.gov
               Plate: L1M9694 row: 1 column: 04
               High quality sequence stop: 733.
FEATURES
  source
    1..832
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:4309876"
    /clone_lib="NIH_MGC_48"
    /tissue_type="Primary B-cells from tonsils (cell line)"
    /lab_host="DH10B (phage-resistant)"
    /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
    Site 2: EcoRI; CDNA made by oligo-dT priming.
    Directionally cloned into EcoRI/XhoI sites using the
    following 5' adaptor: GGCAAGGAGG. Size-selected >500bp
    for average insert size 1.8kb. Library constructed by Ling
    Hong in the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-CDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies).
    Note: this is a NIH_MGC Library."
BASE COUNT      168 a 221 c 228 g 215 t
ORIGIN
Query Match      2.8%; Score 71; DB 12; Length 832;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2050 TCGAATCTCTGACCTGAGTATGATCCACCCCTTGCTCCAAAGTGTGGATTACG 2109
DB 253 TCGAATCTCTGACCTGAGTATGATCCACCCCTTGCTCCAAAGTGTGGATTACG 312
QY 2110 GTGTGAGCCAC 2120
DB 313 GTGTGAGCCAC 323

RESULT 39
BG758454      896 bp mRNA linear EST 15-MAY-2001
LOCUS         602712853F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4853076 5',
DEFINITION    mRNA sequence.
ACCESSION     BG758454
VERSION       BG758454.1 GI:14069107
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 896)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-remail.nih.gov
               Tissue Procurement: ATCC
               CDNA Library Preparation: Ling Hong/Rubin Laboratory
               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LNL at:
               http://image.lnl.gov
               Plate: L1M9694 row: 1 column: 13
               High quality sequence stop: 733.
FEATURES
  source
    1..896
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:4853076"
    /clone_lib="NIH_MGC_48"
    /tissue_type="Primary B-cells from tonsils (cell line)"
    /lab_host="DH10B (phage-resistant)"

```

2.7%; Score 69; DB 17; Length 581;
Identity 100.0%; Pred.No. 0;
Insertions 0; Mismatches 0; Indels 0; Gaps 0;

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-27049222
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the PAPSP/LICP Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gechtml2.pl?L=115&C=115-CT0521-031000-163-CT0283=2000-10-03&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 418.

FEATURES

source

1. 420

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="CT0521"

/dev_stage="Adult"

/note="Organ: Colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196

716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

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FEATURES

source

1. 436

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="RPCT-11-454D13"

/clone_id="RPCT-11"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; RPCT11 Human Male BAC Library"

RPCT11 Human Male BAC Library"

RPCT11 Human Male BAC Library"

RPCT11 Human Male BAC Library"

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RPCT11 Human Male BAC Library"

RPCT11 Human Male BAC Library"

RPCT11 Human Male BAC Library"

FEATURES

source

1. 436

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="RPCT-11-454D13"

/clone_id="RPCT-11"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; RPCT11 Human Male BAC Library"

RPCT11 Human Male BAC Library"

RPCT11 Human Male BAC Library"

RPCT11 Human Male BAC Library"

RPCT11 Human Male BAC Library"

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```

/clone.lib="RPCT-11 Human Male BAC Library"
/sex="male"
/note="vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
BASE COUNT      148 a      123 c      101 g      146 t      13 others
ORIGIN

```

Query Match 2.6%; Score 68; DB 17; Length 531;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2053 AACTCCTGACCTAGGTGATCCACCACCTTGGCTTCCAAAGTGCTGGGATTACAGGTG 2112
 |||||
Db 432 AACCTCGACCTCAGGTGATCCACCACCTTGGCTTCCAAAGTGCTGGGATTACAGGTG 491

QY	2113	TGAGCCAC	2120
Db	492	TGAGCCAC	499

RESULT 47	
A0556467	
LOCUS	20556467
	546 bp
DNA	1:near
	CGS 20-MAY-1998

LOCUS	HS52667.1	546 bp	DNA	linear	GenBank
DEFINITION	HS 5266 B1 C01 77A RPCI-11 Human Male BAC Library Homo sapiens				
ACCESSION	U0556467				
VERSION	U0556467.1	GI:4916199			
KEYWORDS	genomic clone	Plac=812	Col=1	Row=F	DNA sequence.

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

**MEDLINE
COMMENT**

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3007

Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@denton.med.buffalo.edu). Clones may be purchased from

or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate. 812 row. F column. 1

Class: BAC ends
High quality sequence stop: 546.
Location/Qualifiers

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=812 Col=1 Row=F"
```

```

/sex="male"
/notes="Vector: pBAce3.6: Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor"

```

BASE COUNT	135 a	120 c	173 g	108 t	10 others
ECORI methinylase. size selected DNA was cl					
pBACE3.6 vector at EcorI sites"					

ORIGIN	
Query Match	2.6%; Score 68; DB 17; Length 546;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 68; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	372 ATTTCCTCGATGATGTCTCTTGAGTGTCTGCTGAGCAACATGGAAGTCTGCCAG 431
DB	383 ATTTCCTCGATGATGTCTCTTGAGTGTCTGCTGAGCAACATGGGAAGTCTGCCAG 442
QY	432 CAGAAGAA 439
DB	443 CAGAAGAA 450

RESULT 48	
AG144939/C	
10000	
AG144939	
701 bp	
DNA	linear
	GSS 08-TAN-2002

sequence.	ACCESSION	VERSION
AG144939	AG144939	1
CT.16674617	AG144939	1

SOURCE Pan troglodytes male lymphocytes DNA, clone_lib:RPc1-43 chimpanzee Male BAC Library clone:RP43-006B10.T7.

REFERENCE
AUTHORS
1 Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Pan
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.

LINE BAC end sequences of library NCI-1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 701)

TITLE	Author	Journal	Year	Volume	Page
Direct Submission	Totoki, Y., Watanabe, H. and Sakaki, Y.	Journal of Polymer Science, Polymer Chemistry Edition	1977	15	1111

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpbes@gsc.riken.go.jp, URL: <http://hgp.gsc.riken.go.jp/>, www.hgp.gsc.riken.go.jp/)

COMMENT Clones are derived from the chimpanzee BAC library RPTC-43 This BAC end was generated during the R&D process and may have higher chance of cloning than the others

Sequencing: T7
LIBRARY
Vector

```

R.Site 2 : ECORI.
FEATURES      Location/Qualifiers
source      1      701

```

```
/db xref="caxon:9598"  
/clone="RPa3-006B10.T7"  
/sex="male"
```

ORIGIN	BASE COUNT				
	212	a	145	c	159
					g
					185
					t

Query Match	2.6%	Score 68	DB 1	Length 101
Best Local Similarity	100.0%	Pred. No. 0		
Matches 68: Conservative	0	Mismatches	0	Indels
			0	Gaps
				0

Db 194 AACTCTGACTCAGGTGATCCACCACCTTGGCTCCCAAGTGTCTGGATTACAGTG 135

QY	2115	1GAGCCAC	212
Db	134	TGAGCCAC	127

RESULT 49
 BG718999/c 742 bp mRNA linear EST 08-MAY-2001
 LOCUS 602699111F1 NIH MGC_97 Homo sapiens cDNA clone IMAGE:4831083 5',
 DEFINITION mRNA sequence.
 ACCESSION BG718999
 VERSION BG718999
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 742)
 NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshitaki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM10753 row: e column: 04
 High quality sequence stop: 740.
 Location/Qualifiers
 source 1..742
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4831083"
 /clone_1ib="NIH MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pBluescript (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gpcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTT-3',
 size-selected for average insert size 2.2 kb and
 normalized to 10^5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."
 BASE COUNT 232 a 167 c 144 g 199 t
 ORIGIN

Query Match 2.6%; Score 66; DB 12; Length 742;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2055 CTCCTGACCTCAGGTGATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAGGTG 2114
 Db 671 CTCCTGACCTCAGGTGATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAGGTG 612

QY 2115 AGCCAC 2120
 Db 611 AGCCAC 606

RESULT 50
 AQ675390/c 472 bp DNA linear GSS 24-JUN-1999
 LOCUS HS 2151 A1 D03 T7C CIT Approved Human Genomic Sperm Library D Homo
 DEFINITION sapiens genomic clone Plate=2151 Col=5 Row=6, DNA sequence.
 ACCESSION AQ675390
 VERSION AQ675390
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 472)
 AUTHORS Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,
 Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and
 Hood L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@regen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 2151 row: G column: 5
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 472.
 Location/Qualifiers
 source 1..472
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=2151 Col=5 Row=G"
 /clone_1ib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBeloBAC11; BAC clones in
 E-Coli DH10B"
 BASE COUNT 143 a 73 c 95 g 158 t 3 others
 ORIGIN

Query Match 2.5%; Score 65; DB 17; Length 472;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2056 TCCTGACCTCAGGTGATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAGGTG 2115
 Db 356 TCCTGACCTCAGGTGATCCACCCACCTTGCCCTCCCAAGTCTGGATTACAGGTG 297

QY 2116 GCCAC 2120
 Db 296 GCCAC 292

RESULT 51
 AU145455 579 bp mRNA linear EST 05-AUG-2002
 LOCUS AU145455 HEMBA1 Homo sapiens cDNA clone HEMBA1004880 3', mRNA
 DEFINITION sequence.
 ACCESSION AU145455
 VERSION AU145455
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 579)
 Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano
 S. and Iwagaki, T.).
 HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S.,
 Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura
 Y., Nagai, T., Sugano, S., Iwagaki, T.)
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Iwagaki
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986

Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

Source

1. 579
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HEMBA1004880"
 /clone_id="HEMBA1"
 /tissue_type="whole embryo, mainly head"
 /dev_stage="embryo, 10 weeks"
 /note="Vector: PME18SFL3"

BASE COUNT 146 a 133 c 111 g 181 t 8 others

ORIGIN

Query Match 2.5%; Score 65; DB 9; Length 579;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2056 TCCTGACCTAGGTGATCCACCCACCTTGCTCCCAAGCTGGGATTACAGGTGGA 2115
 Db 329 TCCTGACCTAGGTGATCCACCCACCTTGCTCCCAAGCTGGGATTACAGGTGGA 368

QY 2116 GCCAC 2120
 |||||
 Db 389 GCCAC 393

RESULT 52

N22395 LOCUS 448 bp mRNA linear EST 20-DEC-1995
 DEFINITION yw37f08.s1 Morton Fetal Cochlea Homo sapiens cDNA clone
 IMAGE:254439.3 similar to contains Alu repetitive element; mRNA
 sequence.

ACCESSION N22395 GI:1128529
 VERSION N22395
 KEYWORDS EST

SOURCE

human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 448)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Maridis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Scheinberg, K., Soares, M.B., Tan, F., Thierrey-Heg, J., Trevisan, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.

AUTHORS

Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

TITLE

Journal MEDLINE
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

COMMENT

Email: estewatson.wustl.edu
 High quality sequence stops: 346
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 844 Std Error: 0.00
 Seq primer: m3 -40 forward
 High quality sequence stop: 346.

FEATURES

1. 448
 Location/Qualifiers

Source

/organism="Homo sapiens"
 /db_xref="GDB:3891892"
 /db_xref="taxon:9606"
 /clone="IMAGE:254439"
 /clone_id="Morton Fetal Cochlea"

/tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37 of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTCGCGAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTATTTTATTTT 3' "

BASE COUNT 124 a 105 c 94 g 122 t 3 others

ORIGIN

Query Match 2.5%; Score 63; DB 14; Length 448;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2058 CTGACCTAGGTGATCCACCCACCTTGCTCCCAAGCTGGGATTACAGGTGAGC 2117
 Db 214 CTGACCTAGGTGATCCACCCACCTTGCTCCCAAGCTGGGATTACAGGTGAGC 273

QY 2118 CAC 2120
 |||||
 Db 274 CAC 276

RESULT 53
 A0531017 LOCUS 457 bp DNA linear GSS 18-MAY-1999
 DEFINITION RPCI-11-373D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-373D14
 DNA sequence.

ACCESSION A0531017 GI:4843060
 VERSION A0531017
 KEYWORDS GSS.

SOURCE

human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 457)
 Zhao, S., Adams, M.D., Nieman, W., Malek, J., de Jong, P. and Venter
 J.C.

AUTHORS

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other GSSs: RPCI-11-373D14.TV
 Contact: Shaying Zhao, William Nieman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208

TITLE

Email: hbe@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACBAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genet cs (info@resgen.com). BAC end search page:
 http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: T7
 Class: BAC ends.

FEATURES

1. 457
 Location/Qualifiers

Source

/organism="Homo sapiens"
 /db_xref="GDB:7642933"
 /db_xref="taxon:9606"
 /clone="RPCI-11-373D14"
 /clone_id="RPCI-11"
 /sex="Male"
 /cell_type="Tymphocytess"
 /note="Vector: pBAC3.6; site 1: EcoRI; site 2: EcoRI;
 RPCI11 Human Male BAC Library"

BASE COUNT

127 a 79 c 115 g 136 t

ORIGIN

Query Match 2.5%; Score 63; DB 17; Length 457;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2058 CTGACCTGAGTGTATCCACCCAGCTTGAGCTCCCAAGTCTGGAGATTACAGTGTAGC 2117

Db 286 CTGACCTGAGTGTATCCACCCAGCTTGAGCTCCCAAGTCTGGAGATTACAGTGTAGC 227

Qy 2118 CAC 2120

Db 226 CAC 224

RESULT 54

LOCUS

DEFINITION RPT-11-475A11.TV RPT-11 Homo sapiens genomic clone RPT-11-475A11

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 621)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.

TITLE

Use of BAC End Sequences from Library RPT-11 for Sequence-Ready Map Building

JOURNAL

Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208

COMMENT

Email: hbeetigf.org
Clones are derived from the human BAC library RPT-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet. Co. (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html. Seq primer: T7

Class: BAC ends.

FEATURES

source

location/Qualifiers

1..621

/organism="Homo sapiens"

/db_xref="GDB:7682026"

/db_xref="taxon:9606"

/clone="RPT-11-475A11"

/clone_1lb="RPT-11"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBAC3.5; Site_1: EcoRI; Site_2: EcoRI; RPT-11 Homo Male BAC library"

BASE COUNT

132 a

177 c

150 g

162 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 0;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2052 GAACCTGAGTGTATCCACCCAGCTTGAGCTCCCAAGTCTGGAGATTACAGGT 2111

Db 222 GAACCTGAGTGTATCCACCCAGCTTGAGCTCCCAAGTCTGGAGATTACAGGT 281

Qy 2112 GTG 2114

Db 282 GTG 284

RESULT 55

LOCUS

DEFINITION QV1-CT0364-260100-052-g03 CT0364 Homo sapiens cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 433)
Dias Neco, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brumstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.V. and Simpson, A.J.G.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fl=ct2=QV1-CT0364-260100-052-g03&ts=2000-01-26&ts=1)

Seq primer: puc 18 forward
High quality sequence start: 49
High quality sequence stop: 433.

FEATURES

source

location/Qualifiers

1..433

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_1lb="CT0364"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196

716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT

121 a

111 c

108 g

93 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 0;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2059 TGACCTGAGTGTATCCACCCAGCTTGAGCTCCCAAGTCTGGAGATTACAGGT 2118

Db 171 TGACCTGAGTGTATCCACCCAGCTTGAGCTCCCAAGTCTGGAGATTACAGGTAGCC 112

Qy 2119 AC 2120

Db 111 AC 110

RESULT 56

LOCUS

DEFINITION RPT-11-112J16.TV RPT-11 Homo sapiens genomic clone RPT-11-112J16, DNA sequence.

ACCESSION

Qy 2112 GTG 2114

Db 282 GTG 284

VERSION A0343967.1 GI:4168863
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 543)
 AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
 J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other GSSs: RPCI11-112J16.TV
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.
 FEATURES
 source
 Location/Qualifiers
 1..543
 /organism="Homo sapiens"
 /db_xref="GDB:7542855"
 /db_xref="taxon:9606"
 /clone="RPCI-11-112J16"
 /clone_id="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI1 Human Male BAC library"
 BASE COUNT 127 a 138 c 131 g 147 t
 ORIGIN
 Query Match 2.4%; Score 62; DB 17; Length 543;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2059 TGACCTCAGGTATCCACCCACCTTGCCCTCCCAAGTGTGGATTACAGGTGAGCC 2118
 DB 359 TGACCTCAGGTATCCACCCACCTTGCCCTCCCAAGTGTGGATTACAGGTGAGCC 418
 QY 2119 AC 2120
 DB 419 AC 420
 RESULT 57
 A0435006/c 593 bp DNA linear GSS 31-MAR-1999
 LOCUS HS_5114_B2_A08 T7A RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate=690 Col=16 Row=B, DNA sequence.
 ACCESSION A0435006
 VERSION A0435006.1 GI:4546345
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 593)
 AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Research Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
 plate: 690 row: B column: 16
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 593.
 FEATURES
 source
 Location/Qualifiers
 1..593
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=690 Col=16 Row=B"
 /clone_id="RPCI-11 Human Male BAC library"
 /sex="male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAC3.6 vector at EcoRI sites"
 BASE COUNT 150 a 158 c 117 g 142 t 26 others
 ORIGIN
 Query Match 2.4%; Score 62; DB 17; Length 593;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2059 TGACCTCAGGTATCCACCCACCTTGCCCTCCCAAGTGTGGATTACAGGTGAGCC 2118
 DB 337 TGACCTCAGGTATCCACCCACCTTGCCCTCCCAAGTGTGGATTACAGGTGAGCC 278
 QY 2119 AC 2120
 DB 277 AC 276
 RESULT 58
 AM470105 174 bp mRNA linear EST 24-FEB-2000
 LOCUS XR29912.X1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2761606 3'
 DEFINITION similar to contains Alu repetitive element; contains element MER35
 repetitive element; mRNA sequence.
 ACCESSION AM470105
 VERSION AM470105.1 GI:7040211
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 174)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

/MORE- VERVOL: P173D-FAC (FIMATIMMACDA) WITH A MOUNTED

3111c

from ORSSTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT

71 a 57 c 62 g 44 t

ORIGIN

Query Match 2.4%; Score 61; DB 13; Length 234;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

2050 TCGAAGCTCTGAGCTGATGATCCACCCAGCTGCTGCGAAGTGGATTACAG 2109
182 TCGAAGCTCTGAGCTGATGATCCACCCAGCTGCTGCGAAGTGGATTACAG 123

Qy

2110 G 2110
122 G 122

RESULT 61

BS897239

LOCUS BS897239 309 bp mRNA linear EST 06-NOV-2001
DEFINITION HOA60-1-H3.R HOA (Human Osteoarthritic Cartilage) Homo sapiens CDNA

ACCESSION

BS897239

VERSION

BS897239.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 309)

AUTHORS

Kumar, S., Connor, J. R., Dodd, R. A., Halsey, W., Van Horn, M., Mao, J.,
Sathie, G., Mui, P., Agarwal, P., Badger, A. M., Lee, J. C., Gowen, M. and
Lark, M. W.

TITLE

Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries

JOURNAL

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

MEDLINE

21482651

COMMENT

Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5538
Email: sanjay.kumar-1@sk.com
Seq primer: 17.
Location/Qualifiers
1. 309
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/tissue_type="cartilage"
/lab_host="E. coli DH10 B"
/note="vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

BASE COUNT

62 a 93 c 79 g 75 t

ORIGIN

Query Match 2.4%; Score 61; DB 12; Length 309;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

2050 TCGAAGCTCTGAGCTGATGATCCACCCAGCTGCTGCGAAGTGGATTACAG 2109
210 TCGAAGCTCTGAGCTGATGATCCACCCAGCTGCTGCGAAGTGGATTACAG 269

Qy

2110 G 2110
270 G 270

RESULT 62
AA010265
LOCUS 325 bp mRNA linear EST 09-MAY-1997
DEFINITION z10905.at Soares fetal liver spleen INFLS S1 Homo sapiens CDNA
clone IMAGE:430304 3' similar to contains Alu repetitive element
; contains element MER22 repetitive element ;, mRNA sequence.

ACCESSION

AA010265

VERSION

AA010265.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 325)

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M. F., Chiappelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M. B., Tan, F., Thierry-Mieg, J., Trevaekis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE

Genome Res. 6 (9), 807-828 (1996)

JOURNAL

Genome Res. 6 (9), 807-828 (1996)

MEDLINE

9704478

COMMENT

Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1517 Std Error: 0.00
Seq primer: mod.RGA+ET
High quality sequence stop: 274.
Location/Qualifiers
1. 325
/organism="Homo sapiens"
/db_xref="GDB:1330073"
/db_xref="taxon:9606"
/clone_lib="IMAGE:430304"
/clone_lib="Soares_fetal_liver_spleen_INFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pRTT3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5'
ACTGAGAGATTATTAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pRTT3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

63 a 92 c 66 g 97 t 1 others

ORIGIN

Query Match 2.4%; Score 61; DB 9; Length 325;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

2050 TCGAAGCTCTGAGCTGATGATCCACCCAGCTGCTGCGAAGTGGATTACAG 2109
168 TCGAAGCTCTGAGCTGATGATCCACCCAGCTGCTGCGAAGTGGATTACAG 227

Qy

2110 G 2110
228 G 228

RESULT 63
AA93165
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

AA93165 346 bp mRNA linear EST 27-AUG-1998
ct77c09.s1 Soares total fetus Nb2H8 9w Homo sapiens cDNA clone
IMAGE:1622800 3' similar to contains Alu repetitive element, mRNA
sequence.
AA93165
EST.
AA93165.1 GI:3179710
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 346)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1727 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 338.
Location/Qualifiers
1. 346
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1622800"
/clone_1lb="Soares total_fetus_Nb2H8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TCCTACCATCTGAAGCGAGCGCGCTTAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73D vector. Library
went through one round of normalization, and was
constructed by Benito Soares and M. Fatima Bonaldo."

BASE COUNT 78 a 94 c 75 g 99 t

ORIGIN

Query Match 2.4%; Score 61; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAATCTCTGACCTGAGTGATCCACCCACCTTGGCTTCCCAAGTCTGGATTACG 2109
DB 204 TCGAATCTCTGACCTGAGTGATCCACCCACCTTGGCTTCCCAAGTCTGGATTACG 263

QY 2110 G 2110

DB 264 G 264

RESULT 64
AV762430
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AV762430 350 bp mRNA linear EST 19-OCT-2000
AV762430 MDS Homo sapiens cDNA clone MDSBDF09 5', mRNA sequence.
AV762430.1 GI:10920278
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 350)
Gu, J., Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H.,
Gu, Y., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng

TITLE
JOURNAL
COMMENT
FEATURES

Y., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G.,
Yang, Y., Gao, G., Zhang, Q., Chen, S., Han, Z., and Chen, Z.
Homo sapiens cDNA MDS clones
Unpublished (2000)
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hazng@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. 350
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MDSBDF09"
/clone_1lb="MDS"
/issue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/note="Vector: pT73D-Pac; Site_1: SfiI; Site_2: SfiI"

BASE COUNT 93 a 86 c 100 g 71 t

ORIGIN

Query Match 2.4%; Score 61; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAATCTCTGACCTGAGTGATCCACCCACCTTGGCTTCCCAAGTCTGGATTACG 2109
DB 80 TCGAATCTCTGACCTGAGTGATCCACCCACCTTGGCTTCCCAAGTCTGGATTACG 21

QY 2110 G 2110

DB 20 G 20

RESULT 65
AA731898
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

AA731898 377 bp mRNA linear EST 07-FEB-1998
hw71d10.s1 NCI-CCAP GCBI Homo sapiens cDNA clone IMAGE:1252051 3'
similar to contains Alu repetitive element; contains element PTR5
repetitive element; mRNA sequence.
AA731898
EST.
AA731898.1 GI:2752709
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 377)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Benito Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIND at:
www.bio.llnl.gov/bdip/image/image.html
Insert Length: 1654 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 376.
Location/Qualifiers
1. 377
/organism="Homo sapiens"

TITLE 'I.B., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
Unpublished (2000)

JOURNAL Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: john@tigr.org
Place: 286

COMMENT Seq primer: Forward.
Location/Qualifiers

FEATURES
source 1..501
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGE"
/note="Vector: pBluescriptSKm"

BASE COUNT 119 a 128 c 150 g 104 t
ORIGIN

Query Match 2.4%; Score 61; DB 10; Length 501;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAAGCTGACCTGAGTGATCCACCCACCTTGCCCAAGTGTGGATTACAG 2109
Db 188 TCGAAGCTGACCTGAGTGATCCACCCACCTTGCCCAAGTGTGGATTACAG 129

Qy 2110 G 2110
Db 128 G 128

RESULT 73
LOCUS AW753552 568 bp mRNA linear EST 28-APR-2000
DEFINITION PM3-CT0264-151099-001-905 CT0264 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW753552
VERSION AW753552.1 GI:7668484
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 568)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

REFERENCE
AUTHORS
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM3&t2=PM3-CT0264-
151099-001-905&t3=1999-10-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 537.
Location/Qualifiers

FEATURES

source 1..568
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0264"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ONESTES PCR (U.S. Letters Patent Application No. 196
'716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 140 a 118 c 112 g 198 t
ORIGIN

Query Match 2.4%; Score 61; DB 10; Length 568;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAAGCTGACCTGAGTGATCCACCCACCTTGCCCAAGTGTGGATTACAG 2109
Db 164 TCGAAGCTGACCTGAGTGATCCACCCACCTTGCCCAAGTGTGGATTACAG 223

Qy 2110 G 2110
Db 224 G 224

RESULT 74
LOCUS AM806847 613 bp mRNA linear EST 17-MAY-2000
DEFINITION MR0-ST0020-201099-003-b12 ST0020 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM806847
VERSION AM806847.1 GI:7899841
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 613)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

REFERENCE
AUTHORS
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR0-ST0020-201
099-003-b12&t3=1999-10-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 47
High quality sequence stop: 594.
Location/Qualifiers

FEATURES
source 1..613
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/db_xref="taxon:9606"
/clone_lib="ST0020"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products

site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 142 a 149 c 193 g 129 t
ORIGIN

Query Match 2.4%; Score 61; DB 10; Length 613;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2052 GAATCTGACCTGAGTGCACCCACCTGGCTCCCAAGTGTGATTCAGGT 2111
DB 433 GAATCTGACCTGAGTGCACCCACCTGGCTCCCAAGTGTGATTCAGGT 374

QY 2112 G 2112
DB 373 G 373

RESULT 75
LOCUS AV733872/c 618 bp mRNA linear EST 17-OCT-2000

DEFINITION AV733872 cda Homo sapiens cDNA clone cdaSG06 5', mRNA sequence.

ACCESSION AV733872

VERSION AV733872.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Human

Human

Human

Human

Human

Human

Human

Human

Human

Human

Human

Human

Human

Human

Search completed: March 30, 2003, 19:49:22
Job time : 4114 secs

Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

Location/Qualifiers

1. 618

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="cdaSG06"

/clone_id="cda"

/tissue_type="pheochromocytoma"

/dev_stage="Adult"

/lab_host="BM25.8"

/note="vector: pTriplEx2; Site_1: sf1A; Site_2: sf1B"

BASE COUNT 136 a 203 c 142 g 135 t 2 others

ORIGIN

Query Match 2.4%; Score 61; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAATCTGACCTGAGTGCACCCACCTGGCTCCCAAGTGTGATTCAG 2109
DB 563 TCGAATCTGACCTGAGTGCACCCACCTGGCTCCCAAGTGTGATTCAG 504

QY 2110 G 2110
DB 603 G 503